IN THE UNITED STATES DISTRICT COURT
FOR THE WESTERN DISTRICT OF TEXAS
WACO DIVISION

Natera, Inc., Plaintiff, v. Progenity, Inc., Defendant.	Civil Action No. 6:20-cv-532 **JURY TRIAL DEMANDED**

COMPLAINT FOR PATENT INFRINGEMENT

Plaintiff Natera, Inc. ("Natera"), for its Complaint against Defendant Progenity, Inc. ("Progenity" or "Defendant"), alleges as follows:

NATURE OF THE ACTION

1. This is a civil action for infringement of United States Patent Nos. 9,228,234 (the "'234 Patent"); 9,424,392 (the "'392 Patent"); 10,227,652 (the "'652 Patent"); 10,240,202 (the "'202 Patent"); 10,266,893 (the "'893 Patent"); and 10,522,242 (the "'242 Patent") (collectively the "Patents-in-Suit"), arising under the Patent Laws of the United States, 35 U.S.C. §§ 271, *et seq.*

THE PARTIES

2. Natera is a company organized and existing under the laws of Delaware, with its principle place of business at 201 Industrial Rd, San Carlos, California 94070.

3. Founded in 2004, Natera (formerly Gene Security Network) is a pioneering molecular technology company dedicated to improving disease management for reproductive health, oncology, and organ transplantation. For over fifteen years, Natera has been researching

and developing non-invasive methods for analyzing DNA to help patients and doctors manage diseases.

4. Natera is a leading developer of highly accurate solutions for non-invasive prenatal testing ("NIPT"), genetic-carrier screening, and miscarriage testing. Natera's PanoramaTM Prenatal Screen test is a market-leading NIPT test that analyzes a fetus's risk for genetic disorders as early as nine weeks through a simple blood draw from the mother's arm. Panorama is a cell-free DNA ("cfDNA")-based test. Natera is considered the industry leading test in this space, with over two million tests performed commercially, and with more than twenty-six peer-reviewed publications.

5. On information and belief, Progenity is a company organized and existing under the laws of Delaware, with its principle place of business located at 4330 La Jolla Village Drive, Suite 200, San Diego, California, 92122. Progenity is registered to do business in the state of Texas. Progenity has appointed Cogency Global Inc., 1601 Elm St., Suite 4360, Dallas, Texas, 75201 as its agent for service of process.

JURISDICTION AND VENUE

6. This action arises under the patent laws of the United States, including 35 U.S.C. §§ 271, *et. seq*. This Court has subject matter jurisdiction over Plaintiff's claims under 28 U.S.C. §§ 1331 and 1338(a).

7. Venue is proper in this District pursuant to 28 U.S.C. §§ 1391(b), (c), (d) and/or 28 U.S.C. § 1400(b) because Defendant has a permanent and continuous presence in, have committed acts of infringement in, and maintain regular and established places of business in this District.

8. By registering to conduct business in Texas, by having facilities where they regularly conduct business in this judicial District, and by having a registered agent in this judicial

District, Defendant has a permanent and continuous presence and regular and established places of business in the Western District of Texas.

9. Defendant is registered to do business in Texas. (Ex. 1 (registered in TX as "Ascendant MDx, Inc."); Ex. 2 (registration amendment in TX changing the legal name from "Ascendant MDx, Inc." to "Progenity, Inc.")). The purpose of the registration in Texas was so that Defendant could pursue an "Independent clinical laboratory" in Texas. (Ex. 1).

10. Defendant enlisted "National Corporation Research, Ltd." to act as its registered agent in this judicial District. From 2013-2019, Defendant's Texas Franchise Tax Reports identify 800 Brazos, Suite 400, Austin, TX, 78701 as Defendant's registered agent's address. (Exs. 3-9).

11. Defendant is affiliated with Patient Service Centers in this judicial District, including at least 15 affiliated centers in Austin, TX; at least 6 affiliated centers in San Antonio, TX; at least 10 affiliated centers in El Paso, TX; and at least 2 affiliated centers in Midland and Odessa, TX. (Exs. 10-13). For example, Defendant is affiliated with at least the following centers in Austin, TX: Clinical Pathology Laboratories – Bailey Square; Clinical Pathology Laboratories – Medical Arts Square; Open Draw; Clinical Pathology Laboratories – Medical Park Tower; ExamOne Austin; Clinical Pathology Laboratories – Wells Branch; Any Lab Test Now – Austin (two locations); Clinical Pathology Laboratories – Southwest Medical Village; Clinical Pathology Laboratories – James Casey; Clinical Pathology Laboratories – Four Points PSC; Clinical Pathology Laboratories – Medical Oaks Pavilion; Clinical Pathology Laboratories – Renfer Way PSC; Clinical Pathology Laboratories – Ladera Park; and Clinical Pathology Laboratories – Brodie Lane. (Ex. 10). Defendant also is affiliated with at least the following centers in San Antonio, TX: CPL – San Antonio – Somerset; Any Lab Test Now (three locations); CPL – San Antonio – Pecan Plaza; and Stat-X Medical Services, Inc. (Ex. 11). Defendant is affiliated with at least the

following centers in El Paso, TX: CPL – El Paso-Mesa; University Medical Center (UMC) – El Paso; University Medical Center (UMC) – Ysleta; University Medical Center (UMC) – West; CPL – El Paso-Remcon; University Medical Center (UMC) – Northeast; Insurance Medicals of El Paso; CPL – El Paso-Vista Del Sol; University Medical Center (UMC) – Dieter; and University Medical Center (UMC) – East. Defendant is affiliated with at least the two following centers in Odessa and Midland, TX, respectively: CPL – Odessa and CPL – Midland. (Ex. 12). Defendant's affiliated centers collect specimens from patients for testing. (Ex. 13). Upon information and belief, the collected specimens are tested by using the infringing products and/or services.

12. Defendant also has at least 10 employees in this judicial District. For example, Defendant's Chief Operating Officer, Damon Silvestry, represents that he resides and works in Austin, TX. (Ex. 14). Additionally, Defendant's Vice President of Sales and Marketing, Doug Sites; Vice President of Medical Affairs, Christina Settler; Vice President of Sales – Specialty Division, George Gianakopoulos; Business Development Manager, Liz Opalka; Medical Science Liason, Mia Salimbene; and Medical Sales Representative, Matt Cline, represent that they reside and work in Austin, TX. (Exs. 15-20). Defendant has additional employees who represent that they reside and work in Waco, El Paso, and San Antonio, TX. For example, Defendant's Medical Science Liaison, Victoria H.; Business Development Manager, Raul Tolentino; and Business Development Manager, Bethany Moore, represent that they reside and work in Waco, El Paso, and San Antonio, TX, respectively. (Exs. 21-23). On information and belief, these employees of the Defendant operate from one or more established places of business operated by the Defendant.

13. Defendant's employees in this judicial District have responsibilities relating to the infringing products and/or services. For example, as Business Development Manager in San Antonio, TX, Bethany Moore's responsibilities and experience include:

> Promote ***complex, molecular, specialized test***. Plan, develop, and ***manage accounts with gynecologist, oncologist and clinical laboratories to exceed sales targets***. Exceeded sales goals by prospecting new accounts and increasing volume in current accounts.

(Ex. 23 at 1) (emphasis added).

14. As another example, as Vice President of Medical Affairs in Austin, TX, Christina Settler's responsibilities and experience relate to the infringing activities and include, among other things:

> Extensive clinical and commercial experience shaping ***genetic testing products with the ability to provide clinical support to promote market adoption***. Strong business acumen and expertise in genetic testing, clinical affairs, managed care, payer relations, and sales and marketing support.

(Ex. 16 at 1) (emphasis added).

15. Additionally, as Vice President of Sales and Marketing in Austin, TX, Doug Sites' responsibilities and experience relate to the infringing activities and include, among other things:

> Skilled in all areas of healthcare sales and strategic marketing, including selecting, training and motivating professionals for ***complex products***, business development, reimbursement and ***new product introductions***. Proven operational team leader with ***laboratory***, finance, billing, client services, R&D, quality assurance and marketing automation, all integral in achieving revenue goals and driving shareholder value.

(Ex. 15 at 1) (emphasis added).

16. Defendant also has at least one job opening listed in this judicial District. Upon information and belief, this job opening includes responsibilities relating to the infringing products and/or services. For example, Defendant has a job opening for a "Business Development Manager" listed for El Paso, TX. The "Business Development Manager's" responsibilities include, among other things:

> The business development manager will help train new BMDs, meet the sales budget in the territory, manage opportunities and internal resources, and schedule events.

(Ex. 24 at 3).

17. Upon information and belief, Defendant also has presented multiple studies relating to the infringing products and/or services in this judicial District. For example, Defendant presented at least two posters at a scientific meeting in Austin, TX in 2018. (Ex. 25 at 5, https://www.progenity.com/clinical-publications/carrier-testing-real-life). Additionally, Defendant presented at least four posters at two separate scientific meetings in San Antonio, TX in 2019. (*See* Ex. 26 at 1, https://www.progenity.com/news/progenity-presents-data-acg-2019; Ex. 27 at 3, https://www.progenity.com/clinical-publications/hereditary-cancer-risk-more-common-we-thought).

18. Defendant transacts business within this District by using, offering for sale, and/or selling products and/or services that infringe the Patents-in-Suit, including through their website, which is accessible in this District.

19. Defendant is subject to this Court's jurisdiction pursuant to due process and/or the Texas Long Arm Statute due at least to its substantial business in this State and judicial District, including at least regularly doing business through its registered agent in Austin, TX, and engaging in persistent conduct and/or deriving substantial revenue from goods and services provided to customers in the State of Texas, including the Western District of Texas. For example, Defendant conducts business in the District, by at least using, offering for sale, and/or selling products and/or services that practice the claimed inventions of the Patents-in-Suit, including through its website, which are accessible in this District.

20. This Court has personal jurisdiction over Defendant due, *inter alia*, to its continuous presence in, and systematic contact with, this District and its registration in Texas.

Defendant has established minimum contacts within the forum such that the exercise of jurisdiction over Defendant will not offend traditional notions of fair play and substantial justice.

21. Personal jurisdiction exists over Defendant, because Defendant directly and/or through subsidiaries or intermediaries has committed and continues to commit acts of infringement in this District, by among other things, using, offering for sale, and/or selling products and/or services that infringe the Patents-in-Suit, which led to foreseeable harm and injury to Plaintiff.

22. This Court has personal jurisdiction over Defendant in this action because Defendant has committed acts within the Western District of Texas, giving rise to this action and has established minimum contacts with this forum such that the exercise of jurisdiction over the Defendant would not offend traditional notions of fair play and substantial justice. The Defendant, directly and through subsidiaries or intermediaries, has committed and continues to commit acts of infringement in this District by, among other things, using, offering for sale, and/or selling products and/or services that infringe the Patents-in-Suit, which led to foreseeable harm and injury to Plaintiff.

PATENTS-IN-SUIT

23. The ’234 Patent, entitled “Methods for Non-Invasive Prenatal Ploidy Calling,” was duly and legally issued by the United States Patent and Trademark Office on January 5, 2016. The inventors of the patent are Matthew Rabinowitz, Allison Ryan, George Gemelos, Milena Banjevic, and Zachary Demko, and the patent is assigned to Natera. Natera is the exclusive owner of all rights, title, and interest in the ’234 Patent, and has the right to bring this suit to recover damages for any current or past infringement. A copy of the ’234 Patent is attached as Exhibit 28.

24. The ’392 Patent, entitled “System and Method for Cleaning Noisy Genetic Data from Target Individuals Using Genetic Data from Genetically Related Individuals,” was duly and legally issued by the United States Patent and Trademark Office on August 23, 2016. The

inventors of the patent are Matthew Rabinowitz, Milena Banjevic, Zachary Demko, and David Johnson, and the patent is assigned to Natera. Natera is the exclusive owner of all rights, title, and interest in the '392 Patent, and has the right to bring this suit to recover damages for any current or past infringement. A copy of the '392 Patent is attached as Exhibit 29.

25. The '652 Patent, entitled "System and Method for Cleaning Noisy Genetic Data from Target Individuals Using Genetic Data from Genetically Related Individuals," was duly and legally issued by the United States Patent and Trademark Office on March 12, 2019. The inventors of the patent are Matthew Rabinowitz, Milena Banjevic, Zachary Demko, and David Johnson, and the patent is assigned to Natera. Natera is the exclusive owner of all rights, title, and interest in the '652 Patent, and has the right to bring this suit to recover damages for any current or past infringement. A copy of the '652 Patent is attached as Exhibit 30.

26. The '202 Patent, entitled "System and Method for Cleaning Noisy Genetic Data from Target Individuals Using Genetic Data from Genetically Related Individuals," was duly and legally issued by the United States Patent and Trademark Office on March 26, 2019. The inventors of the patent are Matthew Rabinowitz, Milena Banjevic, Zachary Demko, and David Johnson, and the patent is assigned to Natera. Natera is the exclusive owner of all rights, title, and interest in the '202 Patent, and has the right to bring this suit to recover damages for any current or past infringement. A copy of the '202 Patent is attached as Exhibit 31.

27. The '893 Patent, entitled "System and Method for Cleaning Noisy Genetic Data and Determining Chromosome Copy Number," was duly and legally issued by the United States Patent and Trademark Office on April 23, 2019. The inventors of the patent are Matthew Rabinowitz, Milena Banjevic, Zachary Demko, David Johnson, Dusan Kijacic, Dimitri Petrov, Joshua Sweetkind-Singer, and Jing Xu, and the patent is assigned to Natera. Natera is the exclusive

owner of all rights, title, and interest in the '893 Patent, and has the right to bring this suit to recover damages for any current or past infringement. A copy of the '893 Patent is attached as Exhibit 32.

28. The '242 Patent, entitled "Methods for Non-Invasive Prenatal Ploidy Calling," was duly and legally issued by the United States Patent and Trademark Office on December 31, 2019. The inventors of the patent are Matthew Rabinowitz, Allison Ryan, George Gemelos, Milena Banjevic, and Zachary Demko, and the patent is assigned to Natera. Natera is the exclusive owner of all rights, title, and interest in the '242 Patent, and has the right to bring this suit to recover damages for any current or past infringement. A copy of the '242 Patent is attached as Exhibit 33.

29. The '234 Patent is directed to, among other things, novel methods used in the detection of genetic disorders. For example, claim 1 of the '234 Patent recites:

> A method for determining the number of copies of a chromosome or chromosome segment of interest in the genome of a gestating fetus, the method comprising:
> measuring genetic data at a plurality of loci on at least one chromosome that is expected to be disomic in both the mother and the fetus in a mixed sample of DNA comprising fetal DNA and maternal DNA;
> determining a ratio of fetal to maternal DNA in the mixed sample from the measured genetic data at the plurality of loci on the at least one chromosome that is expected to be disomic in both the mother and the fetus;
> measuring genetic data at a plurality of loci on a chromosome or chromosome segment of interest in the mixed sample of DNA;
> creating one or more hypotheses specifying the number of copies of the chromosome or chromosome segment of interest in the genome of the fetus;
> determining, on a computer, the probability of each of the hypotheses using the measured genetic data for the chromosome or chromosome segment of interest and the ratio of fetal to maternal DNA; and
> selecting the hypothesis with the greatest probability, thereby determining the number of copies of the chromosome or chromosome segment of interest in the genome of the fetus.

30. The '392 Patent is directed to, among other things, novel methods used in the detection of genetic disorders. For example, claim 1 of the '392 Patent recites:

> A method for detecting the presence or absence of a chromosomal abnormality in a fetus, the method comprising:

> (a) measuring the amount of genetic material at multiple polymorphic loci on a chromosome or chromosome segment of interest in a sample comprising DNA from the fetus and DNA from the mother of the fetus; wherein the amount of genetic material at a particular polymorphic locus is determined irrespective of the identity of the alleles at that polymorphic locus;
> (b) determining, on a computer, the probability of the presence and the probability of the absence of a chromosomal abnormality in the fetus by comparing the amount from step (a) to either (i) a threshold value or (ii) an expected amount for a particular copy number hypothesis;
> (c) identifying the presence or absence of a chromosomal abnormality in the fetus by selecting the probability most likely to be true; and
> (d) outputting the selected probability as an indication of whether the fetus has a chromosomal abnormality.

31. The ’652 Patent is directed to, among other things, novel methods used in the detection of genetic disorders. For example, claim 1 of the ’652 Patent recites:

> A method for detecting the presence or absence of a chromosomal abnormality in a fetus, the method comprising:
> (a) measuring an amount of genetic material at multiple loci on a chromosome or chromosome segment of interest in a sample comprising cell-free DNA derived from the fetus and from the mother of the fetus, wherein the measuring comprises amplifying at least 70 loci in a single reaction and using microarray or sequencing to detect amplified reaction products, and wherein the multiple loci are loci having alleles with 100% penetrance in the population;
> (b) determining, on a computer, a probability of the presence and a probability of the absence of a chromosomal abnormality in the fetus by comparing the amounts from step (a) to either (i) a threshold value or (ii) an expected amount for a particular copy number hypothesis;
> (c) identifying the presence or absence of a chromosomal abnormality in the fetus by selecting the probability most likely to be true; and
> (d) outputting the selected probability as an indication of whether the fetus has a chromosomal abnormality, thereby detecting the presence or absence of a chromosomal abnormality in a fetus.

32. The ’202 Patent is directed to, among other things, novel methods used in the detection of genetic disorders. For example, claim 1 of the ’202 Patent recites:

> A method for detecting aneuploidy in a fetus, the method comprising:
> (a) measuring the amounts of genetic material at multiple loci on a chromosome or chromosome segment of interest in a sample comprising cell-free DNA derived from the fetus and from the mother of the fetus, wherein the measuring comprises amplifying at least 70 loci in a single reaction and using microarray or sequencing

> to detect amplified reaction products, and wherein the amount of genetic material at a particular locus is determined irrespective of the identity of the alleles at that locus;
> (b) determining, on a computer, the probability of aneuploidy in the fetus by comparing the measured amounts of genetic material to an expected amount for a particular copy number; and
> (c) outputting the selected probability as an indication of whether the fetus has aneuploidy.

33. The ’893 Patent is directed to, among other things, novel methods used in the detection of genetic disorders. For example, claim 1 of the ’893 Patent recites:

> A method for measuring the amounts of fetal chromosome segments in a maternal blood sample, comprising:
> obtaining cell-free DNA comprising fetal and maternal chromosome segments from the maternal blood sample;
> performing universal amplification on the chromosome segments to generate amplified chromosome segments;
> performing clonal amplification on the amplified chromosome segments to generate clonally amplified chromosome segments; and
> measuring the amounts of clonally amplified fetal chromosome segments by performing next-generation sequencing.

34. The ’242 Patent is directed to, among other things, novel methods used in the detection of genetic disorders. For example, claim 1 of the ’242 Patent recites:

> A method for determining the number of copies of a chromosome or chromosome segment of interest in the genome of a gestating fetus, the method comprising:
> measuring genetic data at a plurality of polymorphic loci on at least one chromosome that is expected to be disomic in both the mother and the fetus and a plurality of polymorphic loci on at least chromosome or chromosome segment of interest, which comprises amplifying at least 500 polymorphic loci from a mixed sample comprising DNA derived from the fetus and DNA derived from the mother, wherein the mixed sample is prepared from a maternal blood or plasma sample that comprises free floating fetal and maternal DNA;
> determining a ratio of DNA derived from the fetus to DNA derived from the mother from the measured genetic data at the plurality of polymorphic loci on the at least one chromosome that is expected to be disomic in both the mother and the fetus;
> creating hypotheses specifying the number of copies of the chromosome or chromosome segment of interest in the genome of the fetus;

> determining, on a computer, the probability of each of the hypotheses using the measured genetic data for the chromosome or chromosome segment of interest and the ratio of DNA derived from the fetus to DNA derived from the mother; and selecting the hypothesis with the greatest probability, thereby determining the number of copies of the chromosome or chromosome segment of interest in the genome of the fetus.

PROGENITY'S INFRINGING ACTIVITIES

A. The Accused Innatal Prenatal Screen

35. Progenity was founded in 2010 and launched its Innatal Prenatal Screen in 2015. The Innatal Prenatal Screen is a noninvasive prenatal test offered to women early in pregnancy to screen for risk of fetal chromosomal conditions, such as Down syndrome, trisomy 13, and trisomy 18, and sex chromosome disorders. On April 29, 2019, Progenity announced changes to the Innatal Prenatal Screen with "the latest sequencing technology, improved chemistry, and bioinformatic analysis." (https://www.progenity.com/news/progenity-launches-first-commercially-available-custom-designed-noninvasive-prenatal-test), but did not release what those changes were. In March 2020, Progenity published a paper evaluating the Innatal Prenatal Screen. Ex. 34 (Porreco *et al*.. "Evaluation of a novel screening method for fetal aneuploidy using cell-free DNA in maternal plasma." J. Med.Screen. 2020, Vol. 27(1) 1-8.).

36. According to Progenity's website:

> Cell-free DNA (cfDNA) is analyzed from a maternal blood sample to assess the pregnancy for common chromosome aneuploidies, including trisomy 21 (Down syndrome), trisomy 18, trisomy 13, and sex chromosome abnormalities. This noninvasive screen offers providers and their patients accurate information about the risk for these conditions during pregnancy, as early as 10 weeks' gestation.
>
> The Innatal Prenatal Screen utilizes massively parallel sequencing (MPS) across the whole genome. This method sequences short fragments of DNA, creating millions of reads that are then mapped to the reference genome. The reads are counted to determine whether the sample has extra or missing reads from a particular chromosome. Abnormal dosage indicating aneuploidy is presumed to be fetal in origin. In rare circumstances, there is an alternative explanation.

> Progenity has upgraded the Innatal Prenatal screen with the latest sequencing technology and improved chemistry, demonstrating higher sensitivities than previous versions of the test. Fetal fraction is determined for each sample using a proprietary algorithm.

(Ex. 35, https://www.progenity.com/products/innatal#practice, accessed June 16, 2020).

37. Progenity is currently developing a 4th Generation Innatal Prenatal Screen and anticipates a commercial launch by the end of 2021.

COUNT I

(Infringement of the '234 Patent)

38. Natera incorporates the foregoing paragraphs of this Complaint by reference.

39. The '234 Patent is valid and enforceable.

40. Progenity has infringed, and continues to infringe, one or more claims of the '234 Patent under 35 U.S.C. § 271, either literally and/or under the doctrine of equivalents, by making, using, selling, and/or offering for sale in the United States, and/or importing into the United States, products and/or methods encompassed by those claims, including Progenity's Innatal Prenatal Screen.

41. For example, Progenity infringes at least exemplary claim 1 of the '234 Patent by using the Innatal Prenatal Screen. For example, use of the Innatal Prenatal Screen is a method for determining the number of copies of a chromosome or chromosome segment of interest in the genome of a gestating fetus. Progenity has published a paper on the Innatal product, Porreco *et al*.. "Evaluation of a novel screening method for fetal aneuploidy using cell-free DNA in maternal plasma." J. Med.Screen. 2020, Vol. 27(1) 1-8. The Progenity Innatal Prenatal Screen:

a. measures genetic data at a plurality of loci on at least one chromosome that is expected to be disomic in both the mother and the fetus in a mixed sample of DNA comprising fetal DNA and maternal DNA (*see* Ex. 36 (Progenity U.S. Patent

Application 2019/0309352) at ¶¶ [0037-0039] ("comparing the test ratio to a plurality of reference ratios that are computed based on reference nucleic acid samples isolated from reference subjects without a copy number variation at the target sequences of interest"));

b. determines a ratio of fetal to maternal DNA in the mixed sample from the measured genetic data at the plurality of loci on the at least one chromosome that is expected to be disomic in both the mother and the fetus (*see* Ex. 34 (Porreco *et al.*, "Evaluation of a novel screening method for fetal aneuploidy using cell-free DNA in maternal plasma," J. Med. Screen, 2020 Vol. 27(1) 1-8) at 6 ("A single nucleotide polymorphism-based fetal fraction estimator also was developed."));

c. measures genetic data at a plurality of loci on a chromosome or chromosome segment of interest in the mixed sample of DNA (*see* Ex. 34 (Porreco *et al.*) at Appx. A ("The sequencing data from the Progenity assay also contains information from 1-2000 SNPs."));

d. creates one or more hypotheses specifying the number of copies of the chromosome or chromosome segment of interest in the genome of the fetus (*see* Ex. 34 (Porreco *et al*.) at 6: "A ploidy model and aneuploidy calling algorithm was developed at Progenity, Inc. to determine fetal ploidy for the common trisomies and sex chromosomes from sequencing data generated by the assay. This algorithm is based on a likelihood model that fits the count of unique aligned reads at each MIP site in the genome to produce a per-chromosome estimate of ploidy and its standard error. A T-score (Supplemental Appendix A) representing the ratio of the difference

between the estimated value and the hypothesized value to the standard error is generated for each chromosome interrogated within each sample.");

e. determines, on a computer, the probability of each of the hypotheses using the measured genetic data for the chromosome or chromosome segment of interest and the ratio of fetal to maternal DNA (*see* Ex. 34 (Porreco *et al*.) at Appx. A ("The ploidy model regresses the site-specific counts against a design matrix composed of covariates obtained from the training data. This model results in estimates of ploidy for chromosomes 13, 18, and 21 (Figures S1-S3) and their standard errors."); and

f. selects the hypothesis with the greatest probability, thereby determining the number of copies of the chromosome or chromosome segment of interest in the genome of the fetus (*see* Ex. 34 (Porreco *et al*.) at Appx. A ("A T-value statistic is generated for these autosomes within each sample where the null hypothesis for ploidy is 2 (euploidy) for autosomes. This T-value is a test statistic for deviation from the null hypothesis of euploidy as obtained from our proprietary ploidy model. Under the alternative hypotheses of maternal of fetal nullisomy, trisomy, etc., the expectation of the ploidy is a linear function of the maternal ploidy, fetal ploidy and fetal fraction. . . . A T-value between 5 and 4 indicate that fetal ploidy is statistically indistinguishable from the euploid distribution. A T-value >4 indicates that fetal ploidy is significantly higher than the euploid distribution and is classified as trisomy.").

42. Progenity has had knowledge of the '234 Patent and its infringement since at least the date of this Complaint.

43. Progenity's infringement of the '234 Patent was, and continues to be, willful and deliberate since at least the date of this Complaint.

44. Natera has been and continues to be damaged by Defendant's infringement of the '234 Patent, and will suffer irreparable injury unless the infringement is enjoined by this Court.

45. Defendant's conduct in infringing the '234 Patent renders this case exceptional within the meaning of 35 U.S.C. § 285.

COUNT II

(Infringement of the '392 Patent)

46. Natera incorporates the foregoing paragraphs of this Complaint by reference.

47. The '392 Patent is valid and enforceable.

48. Progenity has infringed, and continues to infringe, one or more claims of the '392 Patent under 35 U.S.C. § 271, either literally and/or under the doctrine of equivalents, by making, using, selling, and/or offering for sale in the United States, and/or importing into the United States, products and/or methods encompassed by those claims, including Progenity's Innatal Prenatal Screen.

49. For example, Progenity infringes at least exemplary claim 1 of the '392 Patent by using the Innatal Prenatal Screen. For example, use of the Innatal Prenatal Screen is a method for detecting the presence or absence of a chromosomal abnormality in a fetus (*see* Ex. 34 (Porreco *et al.*)) that includes:

a. measuring the amount of genetic material at multiple polymorphic loci on a chromosome or chromosome segment of interest in a sample comprising DNA from the fetus and DNA from the mother of the fetus; wherein the amount of genetic material at a particular polymorphic locus is determined irrespective of the identity of the alleles at that polymorphic locus (*see* Ex. 34 (Porreco *et al.*) at 3 ("The

cfDNA test described here uses a novel MIP strategy developed at Progenity, Inc. to enrich and tag specific genomic sequences for next generation sequencing without the need for a highly-multiplexed target capture reaction"); at 5 ("In all, the probe captured ~200,000 sites across the genome. . . ."); and Appx. A at 2 ("The sequencing data from the Progenity assay also contains information from 1-2,000 SNPs with minor allele frequency >0.3%."; "This model results in estimates of ploidy for chromosomes 13, 18, and 21….");

b. determining, on a computer, the probability of the presence and the probability of the absence of a chromosomal abnormality in the fetus by comparing the amount from step (a) to either (i) a threshold value or (ii) an expected amount for a particular copy number hypothesis (*see* Ex. 34 (Porreco *et al*.) at 6 ("A ploidy model and aneuploidy calling algorithm was developed at Progenity, Inc. to determine fetal ploidy for the common trisomies and sex chromosomes from sequencing data generated by the assay. This algorithm is based on a likelihood model that fits the count of unique aligned reads at each MIP site in the genome to produce a per-chromosome estimate of ploidy and its standard error. A T-score (Supplemental Appendix A) representing the ratio of the difference between the estimated value and the hypothesized value to the standard error is generated for each chromosome interrogated within each sample. A single nucleotide polymorphism-based fetal fraction estimator also was developed."); at Appx. A at 1 ("A T-value statistic is generated for these autosomes within each sample where the null hypothesis for ploidy is 2 (euploidy) for autosomes. This T-value is a test statistic for deviation from the null hypothesis of euploidy as obtained from our proprietary ploidy model.

Under the alternative hypotheses of maternal or fetal nullisomy, trisomy, etc., the expectation of the ploidy is a linear function of the maternal ploidy, fetal ploidy and fetal fraction. The model T-value represents the deviation of the estimated ploidy from the euploid expectation divided by the standard error obtained from fitting a generalized linear model."); and Appx. A at 2 ("A T-value between 5 and 4 indicate that fetal ploidy is statistically indistinguishable from the euploid distribution. A T-value > 4 indicates that fetal ploidy is significantly higher than the euploid distribution and is classified as trisomy. Similar methods were used to test chromosome X and Y ploidy (data not shown).");

c. identifying the presence or absence of a chromosomal abnormality in the fetus by selecting the probability most likely to be true (*see* Ex. 34 (Porreco *et al.*) at Appx. A ("The ploidy model regresses the site-specific counts against a design matrix composed of covariates obtained from the training data. This model results in estimates of ploidy for chromosomes 13, 18, and 21 (Figures S1-S3) and their standard errors. A T-value statistic is generated for these autosomes within each sample where the null hypothesis for ploidy is 2 (euploidy) for autosomes. This T-value is a test statistic for deviation from the null hypothesis of euploidy as obtained from our proprietary ploidy model. Under the alternative hypotheses of maternal of fetal nullisomy, trisomy, etc., the expectation of the ploidy is a linear function of the maternal ploidy, fetal ploidy and fetal fraction. . . . A T-value between 5 and 4 indicate that fetal ploidy is statistically indistinguishable from the euploid distribution. A T-value >4 indicates that fetal ploidy is significantly higher than the euploid distribution and is classified as trisomy."); and

d. outputting the selected probability as an indication of whether the fetus has a chromosomal abnormality, thereby detecting the presence or absence of a chromosomal abnormality in a fetus. *See* Ex. 34 (Porreco *et al*.) at Abstract ("Using the new sequencing technology, 1414 samples were analyzed. The findings showed sensitivities and specificities for the common trisomies and the sex chromosome aneuploidies at >99% (Trisomy 21 sensitivity 99.2 CI 95.6–99.2; specificity 99.9 CI 99.6–99.9). Positive predictive values among the trisomies varied from 85.2% (Trisomy 18) to 99.0% (Trisomy 21), reflecting their prevalence rates in the study.")

50. Progenity has had knowledge of the '392 Patent and its infringement since at least the date of this Complaint.

51. Progenity's infringement of the '392 Patent was, and continues to be, willful and deliberate since at least the date of this Complaint.

52. Natera has been and continues to be damaged by Defendant's infringement of the '392 Patent, and will suffer irreparable injury unless the infringement is enjoined by this Court.

53. Defendant's conduct in infringing the '392 Patent renders this case exceptional within the meaning of 35 U.S.C. § 285.

COUNT III

(Infringement of the '652 Patent)

54. Natera incorporates the foregoing paragraphs of this Complaint by reference.

55. The '652 Patent is valid and enforceable.

56. Progenity has infringed, and continues to infringe, one or more claims of the '652 Patent under 35 U.S.C. § 271, either literally and/or under the doctrine of equivalents, by making, using, selling, and/or offering for sale in the United States, and/or importing into the United States,

products and/or methods encompassed by those claims, including Progenity's Innatal Prenatal Screen.

57. For example, Progenity infringes at least exemplary claim 1 of the '652 Patent by using the Innatal Prenatal Screen. For example, use of the Innatal Prenatal Screen is a method for detecting the presence or absence of a chromosomal abnormality in a fetus. The Innatal Prenatal Screen includes:

a. measuring an amount of genetic material at multiple loci on a chromosome or chromosome segment of interest in a sample comprising cell-free DNA derived from the fetus and from the mother of the fetus, wherein the measuring comprises amplifying at least 70 loci in a single reaction and using microarray or sequencing to detect amplified reaction products, and wherein the multiple loci are loci having alleles with 100% penetrance in the population (*see* Ex. 34 (Porreco *et al.*) at 3 ("The cfDNA test described here uses a novel MIP strategy developed at Progenity, Inc. to enrich and tag specific genomic sequences for next generation sequencing without the need for a highly-multiplexed target capture reaction"); at 5 ("In all, the probe captured ~200,000 sites across the genome. . . ."); and Appx. A at 2 ("The sequencing data from the Progenity assay also contains information from 1-2,000 SNPs with minor allele frequency >0.3%."; "This model results in estimates of ploidy for chromosomes 13, 18, and 21….");

b. determining, on a computer, a probability of the presence and a probability of the absence of a chromosomal abnormality in the fetus by comparing the amounts from step (a) to either (i) a threshold value or (ii) an expected amount for a particular copy number hypothesis(*see* Ex. 34 (Porreco *et al.*) at 6 ("A ploidy model and

aneuploidy calling algorithm was developed at Progenity, Inc. to determine fetal ploidy for the common trisomies and sex chromosomes from sequencing data generated by the assay. This algorithm is based on a likelihood model that fits the count of unique aligned reads at each MIP site in the genome to produce a per-chromosome estimate of ploidy and its standard error. A T-score (Supplemental Appendix A) representing the ratio of the difference between the estimated value and the hypothesized value to the standard error is generated for each chromosome interrogated within each sample. A single nucleotide polymorphism-based fetal fraction estimator also was developed."); at Appx. A at 1 ("A T-value statistic is generated for these autosomes within each sample where the null hypothesis for ploidy is 2 (euploidy) for autosomes. This T-value is a test statistic for deviation from the null hypothesis of euploidy as obtained from our proprietary ploidy model. Under the alternative hypotheses of maternal or fetal nullisomy, trisomy, etc., the expectation of the ploidy is a linear function of the maternal ploidy, fetal ploidy and fetal fraction. The model T-value represents the deviation of the estimated ploidy from the euploid expectation divided by the standard error obtained from fitting a generalized linear model."); and Appx. A at 2 ("A T-value between 5 and 4 indicate that fetal ploidy is statistically indistinguishable from the euploid distribution. A T-value > 4 indicates that fetal ploidy is significantly higher than the euploid distribution and is classified as trisomy. Similar methods were used to test chromosome X and Y ploidy (data not shown).");

c. identifying the presence or absence of a chromosomal abnormality in the fetus by selecting the probability most likely to be true (*see* Ex. 34 (Porreco *et al.*) at Appx.

A ("The ploidy model regresses the site-specific counts against a design matrix composed of covariates obtained from the training data. This model results in estimates of ploidy for chromosomes 13, 18, and 21 (Figures S1-S3) and their standard errors. A T-value statistic is generated for these autosomes within each sample where the null hypothesis for ploidy is 2 (euploidy) for autosomes. This T-value is a test statistic for deviation from the null hypothesis of euploidy as obtained from our proprietary ploidy model. Under the alternative hypotheses of maternal of fetal nullisomy, trisomy, etc., the expectation of the ploidy is a linear function of the maternal ploidy, fetal ploidy and fetal fraction. . . . A T-value between 5 and 4 indicate that fetal ploidy is statistically indistinguishable from the euploid distribution. A T-value >4 indicates that fetal ploidy is significantly higher than the euploid distribution and is classified as trisomy."); and

d. outputting the selected probability as an indication of whether the fetus has a chromosomal abnormality, thereby detecting the presence or absence of a chromosomal abnormality in a fetus. *See* Ex. 34 (Porreco *et al*.) at Abstract ("Using the new sequencing technology, 1414 samples were analyzed. The findings showed sensitivities and specificities for the common trisomies and the sex chromosome aneuploidies at >99% (Trisomy 21 sensitivity 99.2 CI 95.6–99.2; specificity 99.9 CI 99.6–99.9). Positive predictive values among the trisomies varied from 85.2% (Trisomy 18) to 99.0% (Trisomy 21), reflecting their prevalence rates in the study.")

58. Progenity has had knowledge of the '652 Patent and its infringement since at least the date of this Complaint.

59. Progenity's infringement of the '652 Patent was, and continues to be, willful and deliberate since at least the date of this Complaint.

60. Natera has been and continues to be damaged by Defendant's infringement of the '652 Patent, and will suffer irreparable injury unless the infringement is enjoined by this Court.

61. Defendant's conduct in infringing the '652 Patent renders this case exceptional within the meaning of 35 U.S.C. § 285.

COUNT IV

(Infringement of the '202 Patent)

62. Natera incorporates the foregoing paragraphs of this Complaint by reference.

63. The '202 Patent is valid and enforceable.

64. Progenity has infringed, and continues to infringe, one or more claims of the '202 Patent under 35 U.S.C. § 271, either literally and/or under the doctrine of equivalents, by making, using, selling, and/or offering for sale in the United States, and/or importing into the United States, products and/or methods encompassed by those claims, including Progenity's Innatal Prenatal Screen.

65. For example, Progenity infringes at least exemplary claim 1 of the '202 Patent by using the Innatal Prenatal Screen. For example, use of the Innatal Prenatal Screen is a method for detecting aneuploidy in a fetus, and includes:

a. measuring the amounts of genetic material at multiple loci on a chromosome or chromosome segment of interest in a sample comprising cell-free DNA derived from the fetus and from the mother of the fetus, wherein the measuring comprises amplifying at least 70 loci in a single reaction and using microarray or sequencing to detect amplified reaction products, and wherein the amount of genetic material at a particular locus is determined irrespective of the identity of the alleles at that

locus (*see* Ex. 34 (Porreco *et al.*) at 3 ("The cfDNA test described here uses a novel MIP strategy developed at Progenity, Inc. to enrich and tag specific genomic sequences for next generation sequencing without the need for a highly-multiplexed target capture reaction"); at 5 ("In all, the probe captured ~200,000 sites across the genome. . . ."); and Appx. A at 2 ("The sequencing data from the Progenity assay also contains information from 1-2,000 SNPs with minor allele frequency >0.3%."; "This model results in estimates of ploidy for chromosomes 13, 18, and 21….");

b. determining, on a computer, the probability of aneuploidy in the fetus by comparing the measured amounts of genetic material to an expected amount for a particular copy number (*see* Ex. 34 (Porreco *et al.*) at 6 ("A ploidy model and aneuploidy calling algorithm was developed at Progenity, Inc. to determine fetal ploidy for the common trisomies and sex chromosomes from sequencing data generated by the assay. This algorithm is based on a likelihood model that fits the count of unique aligned reads at each MIP site in the genome to produce a per-chromosome estimate of ploidy and its standard error. A T-score (Supplemental Appendix A) representing the ratio of the difference between the estimated value and the hypothesized value to the standard error is generated for each chromosome interrogated within each sample. A single nucleotide polymorphism-based fetal fraction estimator also was developed."); at Appx. A at 1 ("A T-value statistic is generated for these autosomes within each sample where the null hypothesis for ploidy is 2 (euploidy) for autosomes. This T-value is a test statistic for deviation from the null hypothesis of euploidy as obtained from our proprietary ploidy model. Under the alternative hypotheses of maternal or fetal nullisomy, trisomy, etc., the expectation of the

ploidy is a linear function of the maternal ploidy, fetal ploidy and fetal fraction. The model T-value represents the deviation of the estimated ploidy from the euploid expectation divided by the standard error obtained from fitting a generalized linear model."); and Appx. A at 2 ("A T-value between 5 and 4 indicate that fetal ploidy is statistically indistinguishable from the euploid distribution. A T-value > 4 indicates that fetal ploidy is significantly higher than the euploid distribution and is classified as trisomy. Similar methods were used to test chromosome X and Y ploidy (data not shown)."); and

c. outputting the selected probability as an indication of whether the fetus has aneuploidy. *See* Ex. 34 (Porreco *et al*.) at Abstract ("Using the new sequencing technology, 1414 samples were analyzed. The findings showed sensitivities and specificities for the common trisomies and the sex chromosome aneuploidies at >99% (Trisomy 21 sensitivity 99.2 CI 95.6–99.2; specificity 99.9 CI 99.6–99.9). Positive predictive values among the trisomies varied from 85.2% (Trisomy 18) to 99.0% (Trisomy 21), reflecting their prevalence rates in the study.")

66. Progenity has had knowledge of the '202 Patent and its infringement since at least the date of this Complaint.

67. Progenity's infringement of the '202 Patent was, and continues to be, willful and deliberate since at least the date of this Complaint.

68. Natera has been and continues to be damaged by Defendant's infringement of the '202 Patent, and will suffer irreparable injury unless the infringement is enjoined by this Court.

69. Defendant's conduct in infringing the '202 Patent renders this case exceptional within the meaning of 35 U.S.C. § 285.

COUNT V

(Infringement of the '893 Patent)

70. Natera incorporates the foregoing paragraphs of this Complaint by reference.

71. The '893 Patent is valid and enforceable.

72. Progenity has infringed, and continues to infringe, one or more claims of the '893 Patent under 35 U.S.C. § 271, either literally and/or under the doctrine of equivalents, by making, using, selling, and/or offering for sale in the United States, and/or importing into the United States, products and/or methods encompassed by those claims, including Progenity's Innatal Prenatal Screen.

73. For example, Progenity infringes at least exemplary claim 1 of the '893 Patent by using the Innatal Prenatal Screen. For example, use of the Innatal Prenatal Screen is a method for measuring the amounts of fetal chromosome segments in a maternal blood sample, that includes:

a. obtaining cell-free DNA comprising fetal and maternal chromosome segments from the maternal blood sample (*see* Ex. 34 (Porreco *et al.*) at Abstract ("Objective: To evaluate the test performance of a novel sequencing technology using molecular inversion probes applied to cell-free DNA screening for fetal aneuploidy."); and 3 ("Venous blood (approximately 20mL) was collected from study participants. . . .");

b. performing universal amplification on the chromosome segments to generate amplified chromosome segments (*see* Ex. 34 (Porreco *et al.*) at 5 ("The single stranded circular DNA generated from the capture protocol (Figure 1) was used as template in a universal PCR reaction containing primers that bind to the MIP backbone.");

c. performing clonal amplification on the amplified chromosome segments to generate clonally amplified chromosome segments (*see* Ex. 34 (Porreco *et al.*) at 5-6 ("PCR product libraries were purified . . . and samples were pooled into a multiplexed sequencing library (including controls). The library was diluted to an appropriate concentration for patterned flow cell clustering on a NovaSeq 6000. . . ."); and

d. measuring the amounts of clonally amplified fetal chromosome segments by performing next-generation sequencing. *See* Ex. 34 (Porreco *et al.*) at 3 ("The cfDNA test described here uses a novel MIP strategy developed at Progenity, Inc. to enrich and tag specific genomic sequences for next generation sequencing without the need for a highly-multiplexed target capture reaction")

74. Progenity has had knowledge of the '893 Patent and its infringement since at least the date of this Complaint.

75. Progenity's infringement of the '893 Patent was, and continues to be, willful and deliberate since at least the date of this Complaint.

76. Natera has been and continues to be damaged by Defendant's infringement of the '893 Patent, and will suffer irreparable injury unless the infringement is enjoined by this Court.

77. Defendant's conduct in infringing the '893 Patent renders this case exceptional within the meaning of 35 U.S.C. § 285.

COUNT VI

(Infringement of the '242 Patent)

78. Natera incorporates the foregoing paragraphs of this Complaint by reference.

79. The '242 Patent is valid and enforceable.

80. Progenity has infringed, and continues to infringe, one or more claims of the ’242 Patent under 35 U.S.C. § 271, either literally and/or under the doctrine of equivalents, by making, using, selling, and/or offering for sale in the United States, and/or importing into the United States, products and/or methods encompassed by those claims, including Progenity’s Innatal Prenatal Screen.

81. For example, Progenity infringemes at least exemplary claim 1 of the ’242 Patent by using the Innatal Prenatal Screen. For example, use of the Innatal Prenatal Screen is a method for determining the number of copies of a chromosome or chromosome segment of interest in the genome of a gestating fetus. The test includes:

a. measuring genetic data at a plurality of polymorphic loci on at least one chromosome that is expected to be disomic in both the mother and the fetus and a plurality of polymorphic loci on at least chromosome or chromosome segment of interest, which comprises amplifying at least 500 polymorphic loci from a mixed sample comprising DNA derived from the fetus and DNA derived from the mother, wherein the mixed sample is prepared from a maternal blood or plasma sample that comprises free floating fetal and maternal DNA (*see* Ex. 34 (Porreco *et al.*) at 5 (“In all, the probe captured ~200,000 sites across the genome. . . .”); and Appx. A at 2 (“The sequencing data from the Progenity assay also contains information from 1-2,000 SNPs with minor allele frequency >0.3%.”; “This model results in estimates of ploidy for chromosomes 13, 18, and 21….”);

b. determining a ratio of DNA derived from the fetus to DNA derived from the mother from the measured genetic data at the plurality of polymorphic loci on the at least one chromosome that is expected to be disomic in both the mother and the fetus

(*see* Ex. 34 (Porreco *et al.*) at 6 ("A single nucleotide polymorphism-based fetal fraction estimator also was developed.”));

c. creating hypotheses specifying the number of copies of the chromosome or chromosome segment of interest in the genome of the fetus (*see* Ex. 34 (Porreco *et al.*) at 6: "A ploidy model and aneuploidy calling algorithm was developed at Progenity, Inc. to determine fetal ploidy for the common trisomies and sex chromosomes from sequencing data generated by the assay. This algorithm is based on a likelihood model that fits the count of unique aligned reads at each MIP site in the genome to produce a per-chromosome estimate of ploidy and its standard error. A T-score (Supplemental Appendix A) representing the ratio of the difference between the estimated value and the hypothesized value to the standard error is generated for each chromosome interrogated within each sample.”);

d. determining, on a computer, the probability of each of the hypotheses using the measured genetic data for the chromosome or chromosome segment of interest and the ratio of DNA derived from the fetus to DNA derived from the mother (*see* Ex. 34 (Porreco *et al.*) at 6 ("A ploidy model and aneuploidy calling algorithm was developed at Progenity, Inc. to determine fetal ploidy for the common trisomies and sex chromosomes from sequencing data generated by the assay. This algorithm is based on a likelihood model that fits the count of unique aligned reads at each MIP site in the genome to produce a per-chromosome estimate of ploidy and its standard error. A T-score (Supplemental Appendix A) representing the ratio of the difference between the estimated value and the hypothesized value to the standard error is generated for each chromosome interrogated within each sample. A single

nucleotide polymorphism-based fetal fraction estimator also was developed."); at Appx. A at 1 ("A T-value statistic is generated for these autosomes within each sample where the null hypothesis for ploidy is 2 (euploidy) for autosomes. This T-value is a test statistic for deviation from the null hypothesis of euploidy as obtained from our proprietary ploidy model. Under the alternative hypotheses of maternal or fetal nullisomy, trisomy, etc., the expectation of the ploidy is a linear function of the maternal ploidy, fetal ploidy and fetal fraction. The model T-value represents the deviation of the estimated ploidy from the euploid expectation divided by the standard error obtained from fitting a generalized linear model."); and Appx. A at 2 ("A T-value between 5 and 4 indicate that fetal ploidy is statistically indistinguishable from the euploid distribution. A T-value > 4 indicates that fetal ploidy is significantly higher than the euploid distribution and is classified as trisomy. Similar methods were used to test chromosome X and Y ploidy (data not shown)."); and

e. selecting the hypothesis with the greatest probability, thereby determining the number of copies of the chromosome or chromosome segment of interest in the genome of the fetus. *See* Ex. 34 (Porreco *et al.*) at Appx. A ("The ploidy model regresses the site-specific counts against a design matrix composed of covariates obtained from the training data. This model results in estimates of ploidy for chromosomes 13, 18, and 21 (Figures S1-S3) and their standard errors. A T-value statistic is generated for these autosomes within each sample where the null hypothesis for ploidy is 2 (euploidy) for autosomes. This T-value is a test statistic for deviation from the null hypothesis of euploidy as obtained from our proprietary

> ploidy model. Under the alternative hypotheses of maternal of fetal nullisomy, trisomy, etc., the expectation of the ploidy is a linear function of the maternal ploidy, fetal ploidy and fetal fraction. . . . A T-value between 5 and 4 indicate that fetal ploidy is statistically indistinguishable from the euploid distribution. A T-value >4 indicates that fetal ploidy is significantly higher than the euploid distribution and is classified as trisomy.")

82. Progenity has had knowledge of the '242 Patent and its infringement since at least the date of this Complaint.

83. Progenity's infringement of the '242 Patent was, and continues to be, willful and deliberate since at least the date of this Complaint.

84. Natera has been and continues to be damaged by Defendant's infringement of the '242 Patent, and will suffer irreparable injury unless the infringement is enjoined by this Court.

85. Defendant's conduct in infringing the '242 Patent renders this case exceptional within the meaning of 35 U.S.C. § 285.

PRAYER FOR RELIEF

WHEREFORE, Natera prays for judgment as follows:

A. That Progenity has infringed each of the Patents-in-Suit;

B. That Progenity's infringement of each of the Patents-in-Suit has been willful;

C. That Natera be awarded an order enjoining Progenity and its officers, directors, agents, servants, affiliates, employees, divisions, subsidiaries, parents, and all other acting in active concert therewith from further infringement of the Patents-in-Suit;

D. That Natera be awarded all damages adequate to compensate it for Defendant's past infringement and any continuing or future infringement of the Patents-in-Suit up until the date

such judgment is entered, including pre- and post-judgment interest, costs, and disbursements as justified under 35 U.S.C. § 284;

E. That any award of damages be enhanced under 35 U.S.C. § 284 as result of Progenity's willful infringement;

F. That this case by declared an exceptional case within the meaning of 35 U.S.C. §285 and that Natera be awarded the attorney fees, costs, and expenses incurred in connection with this action;

G. That Natera be awarded costs and expenses in this action; and

H. That Natera be awarded such other and further relief at law or equity as this Court deems just and proper.

DEMAND FOR JURY TRIAL

Pursuant to Rule 38(b) of the Federal Rules of Civil Procedure, Plaintiff Natera demands a trial by jury on all issues so triable.

Dated: June 17, 2020

Respectfully submitted,

/s/*Stephen M. Hash*

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